

Figure 2

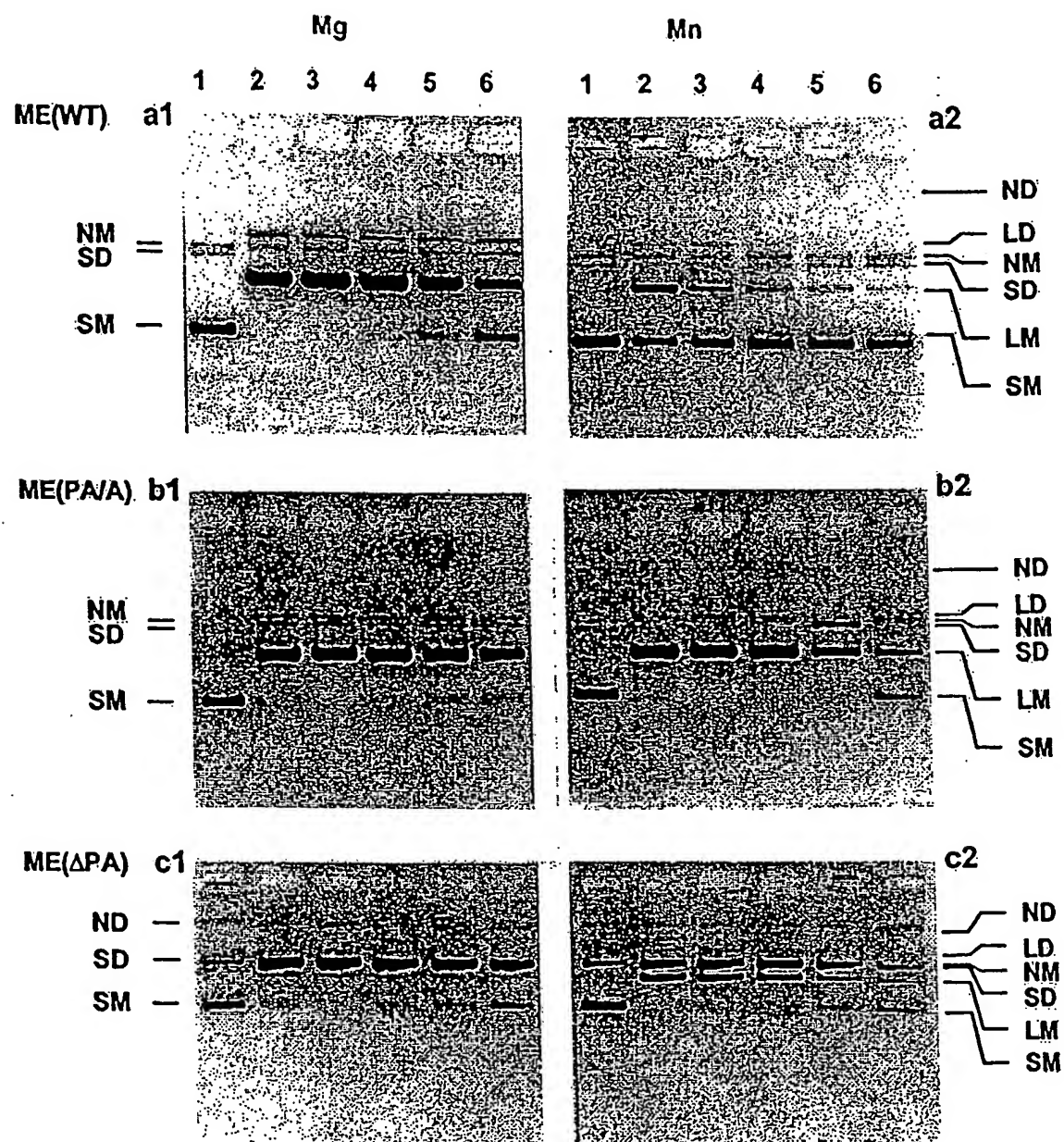


Figure 3

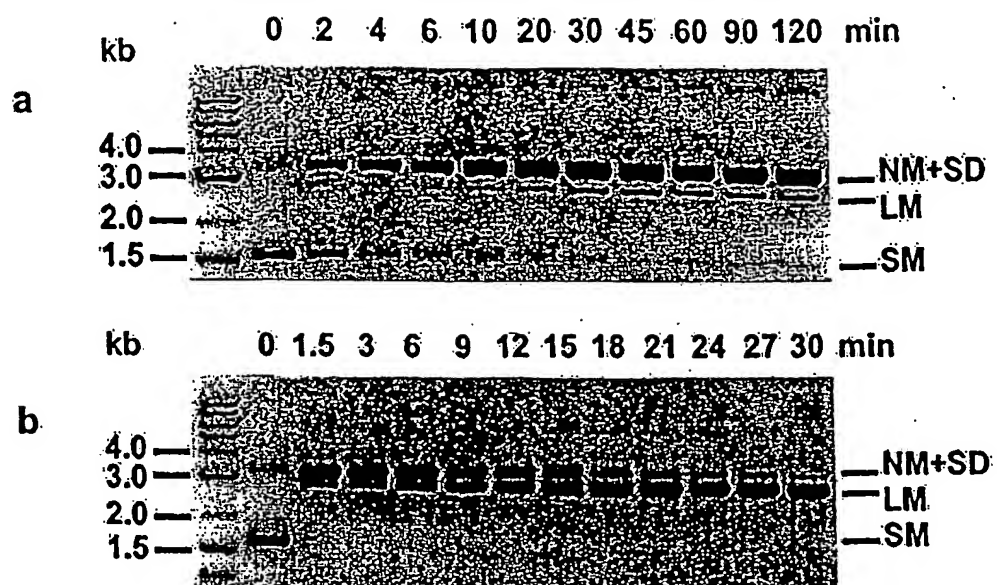


Figure 4

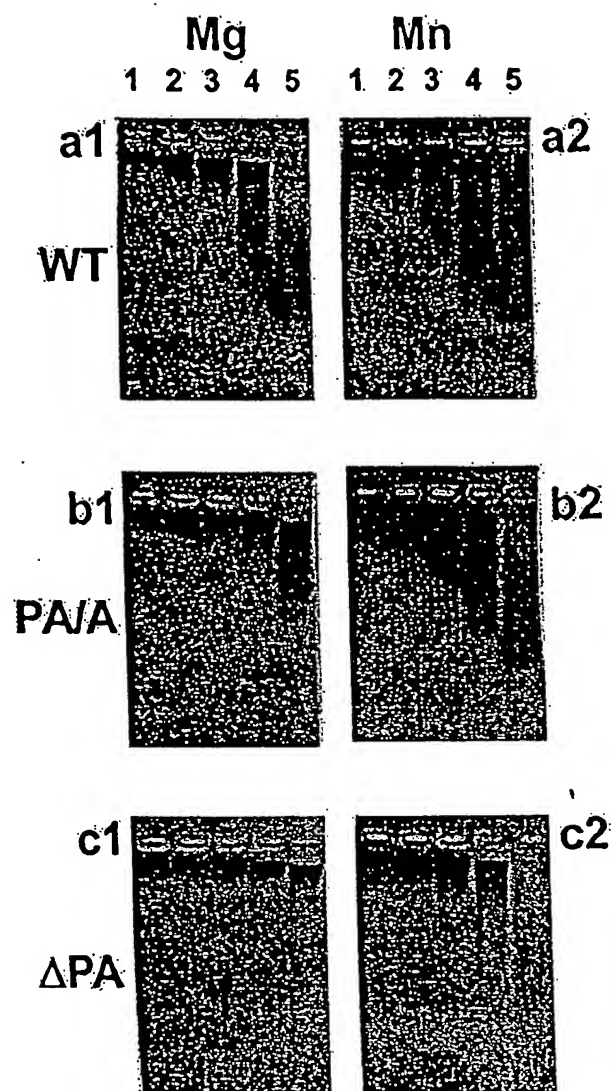


Figure 5A

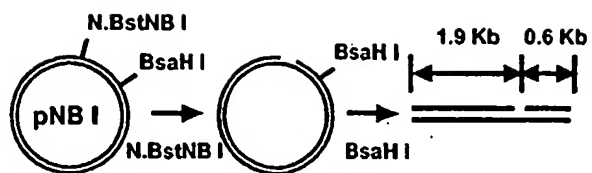


Figure 5B

| | | | | | | |
|-----------|---|---|---|---|---|---|
| N.BstNB I | - | + | + | + | - | - |
| BsaH I | - | - | + | + | + | + |
| ME(PA/A) | - | - | - | + | - | + |

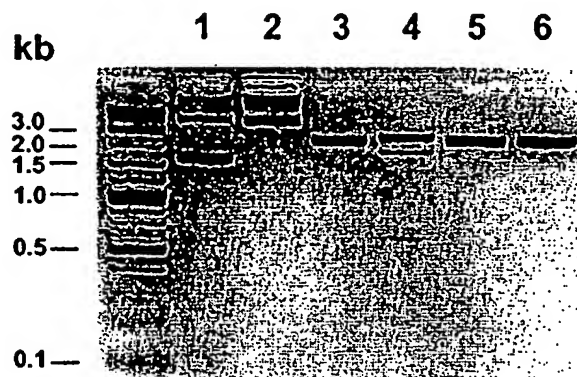
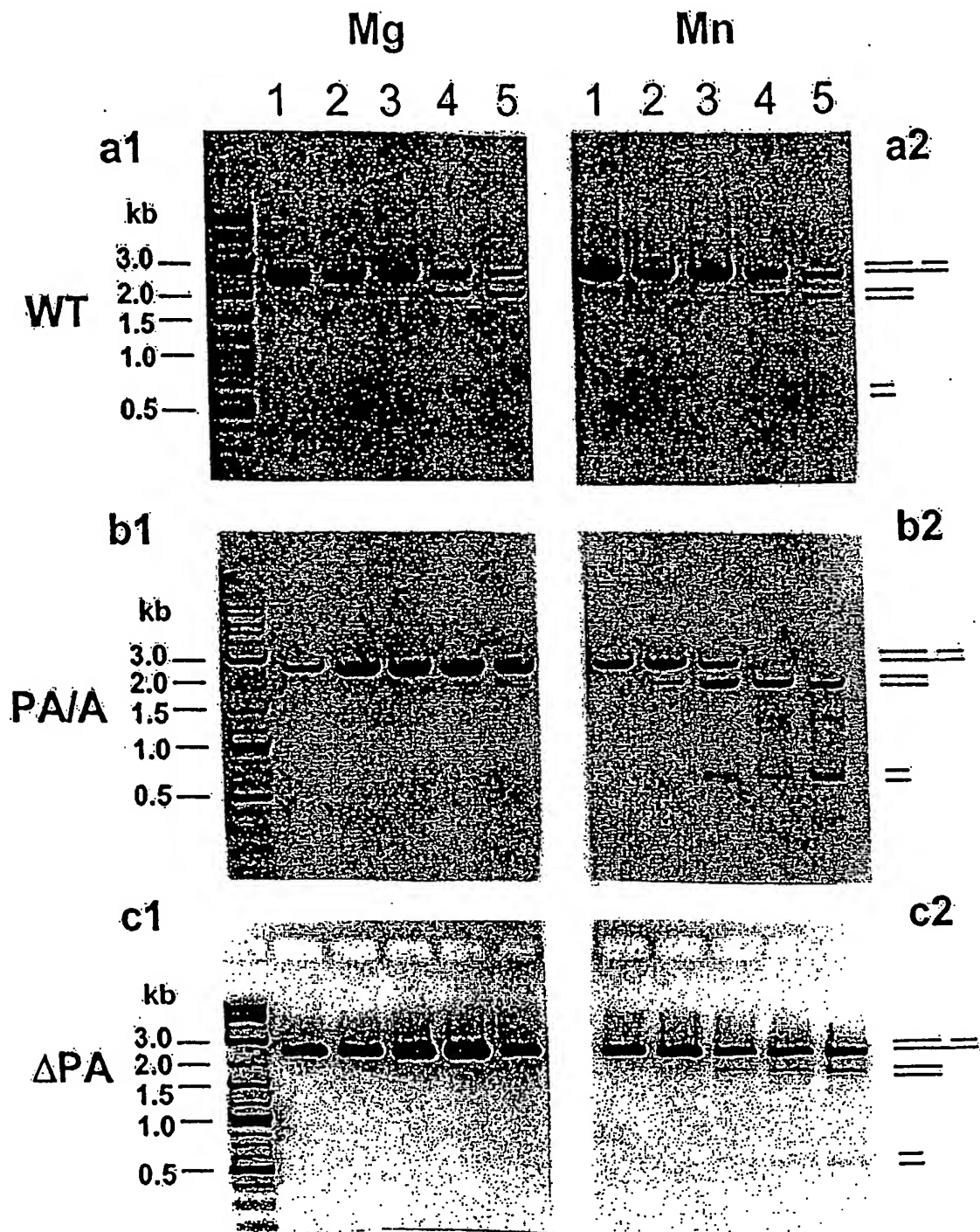


Figure 6



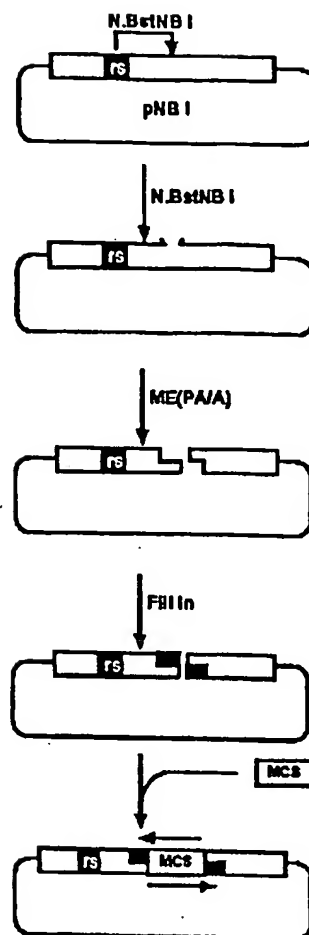


Figure 7.

Figure 8.

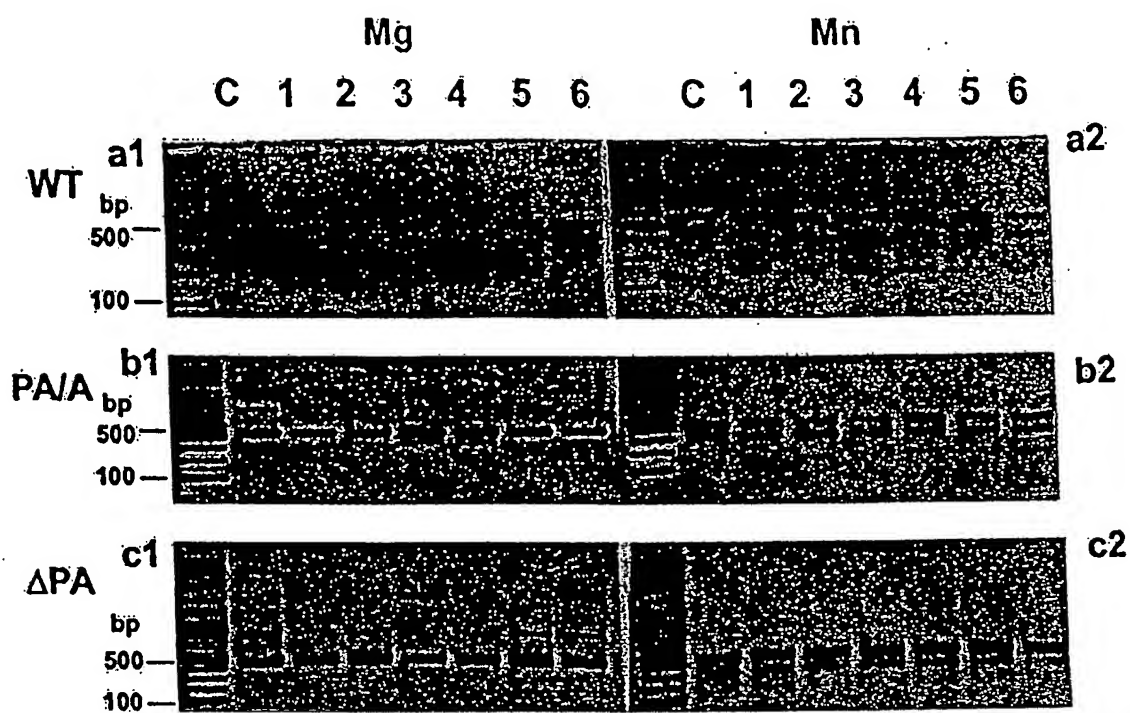
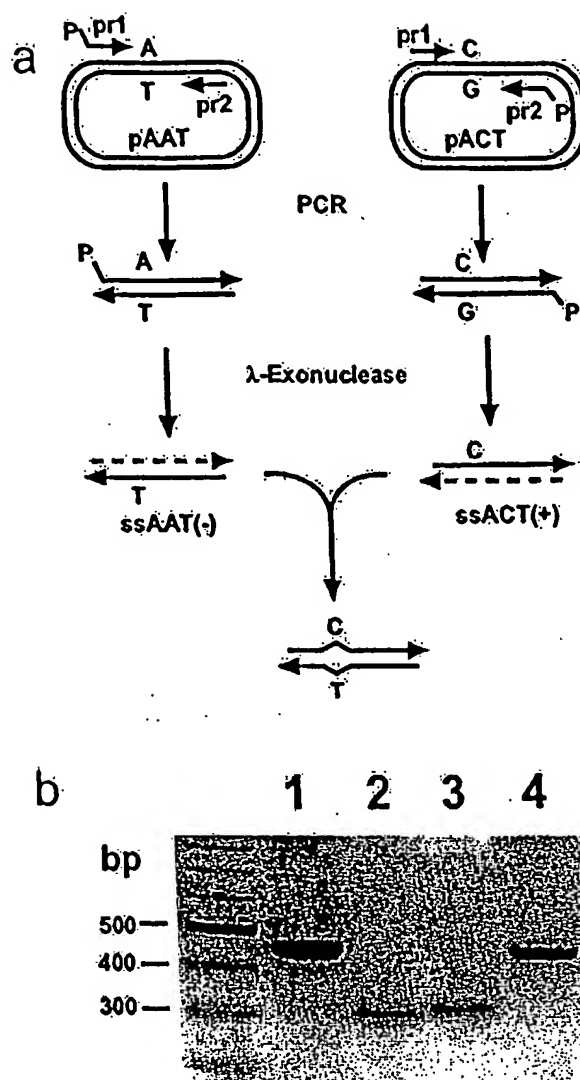
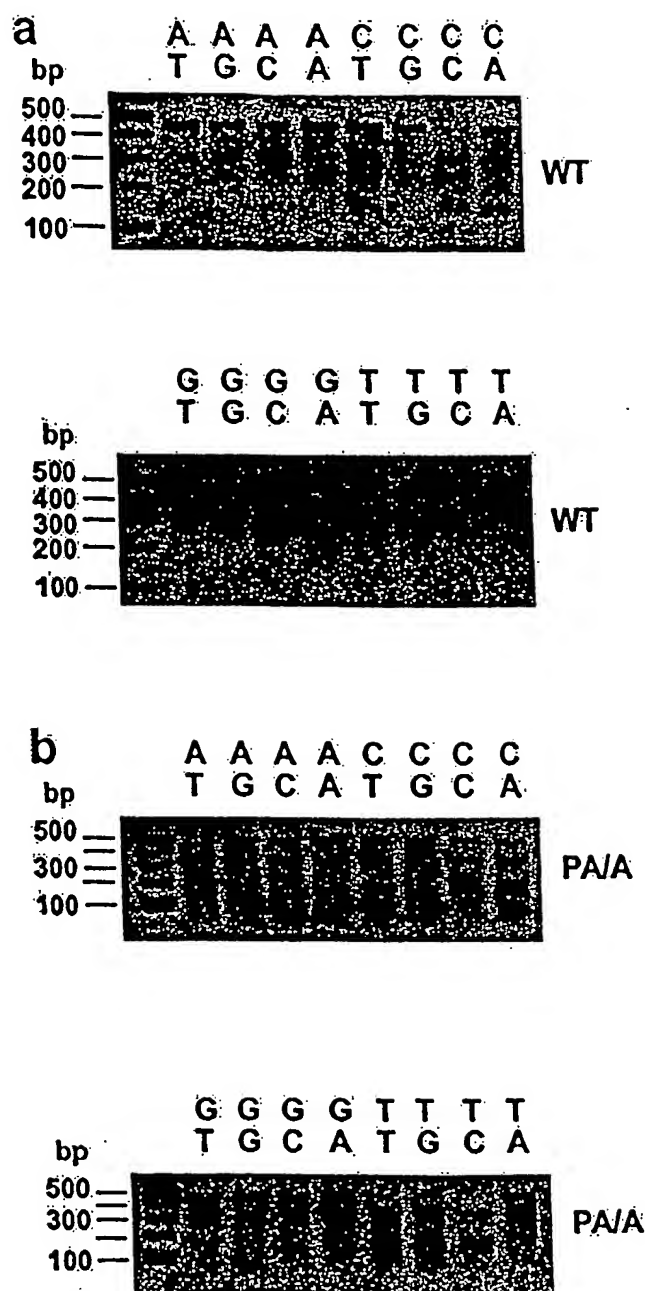


Figure 9.



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Figure 10.



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Figure 11.

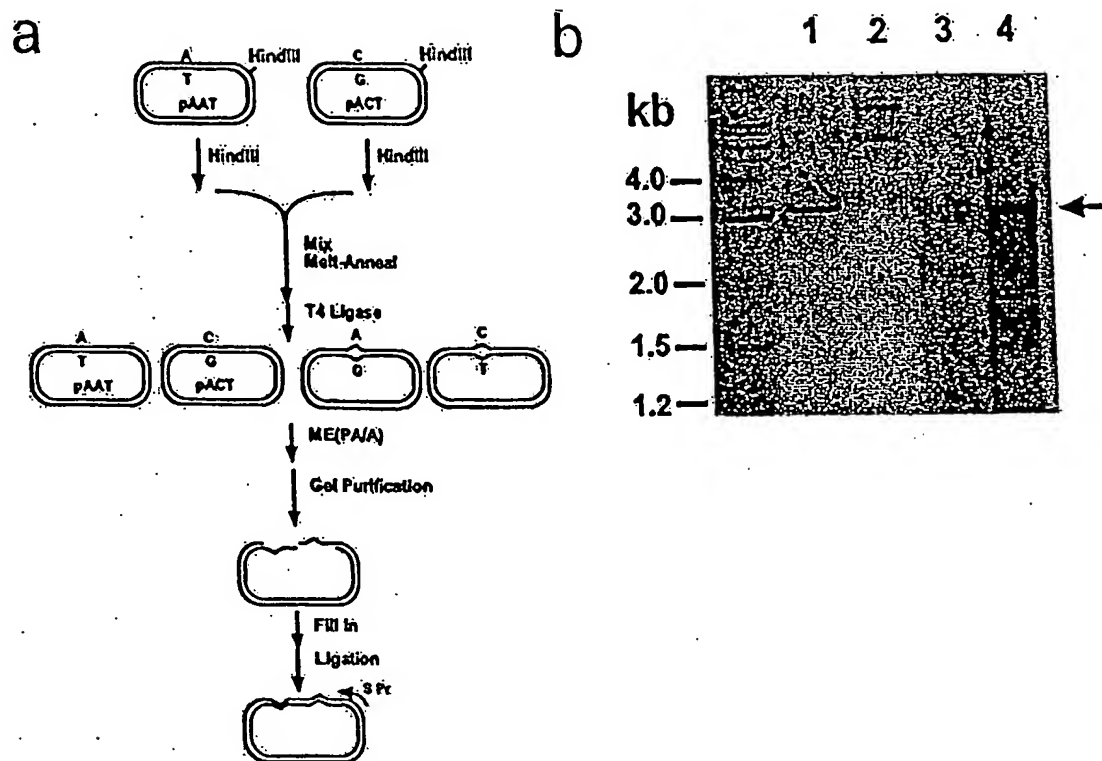
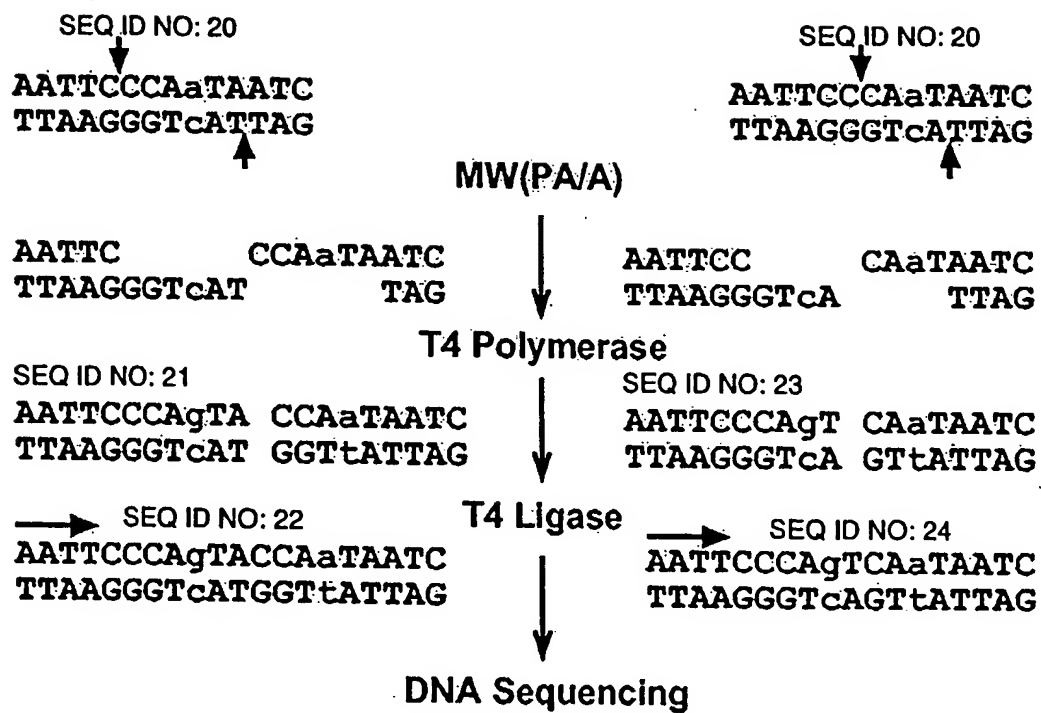


Figure 11 C



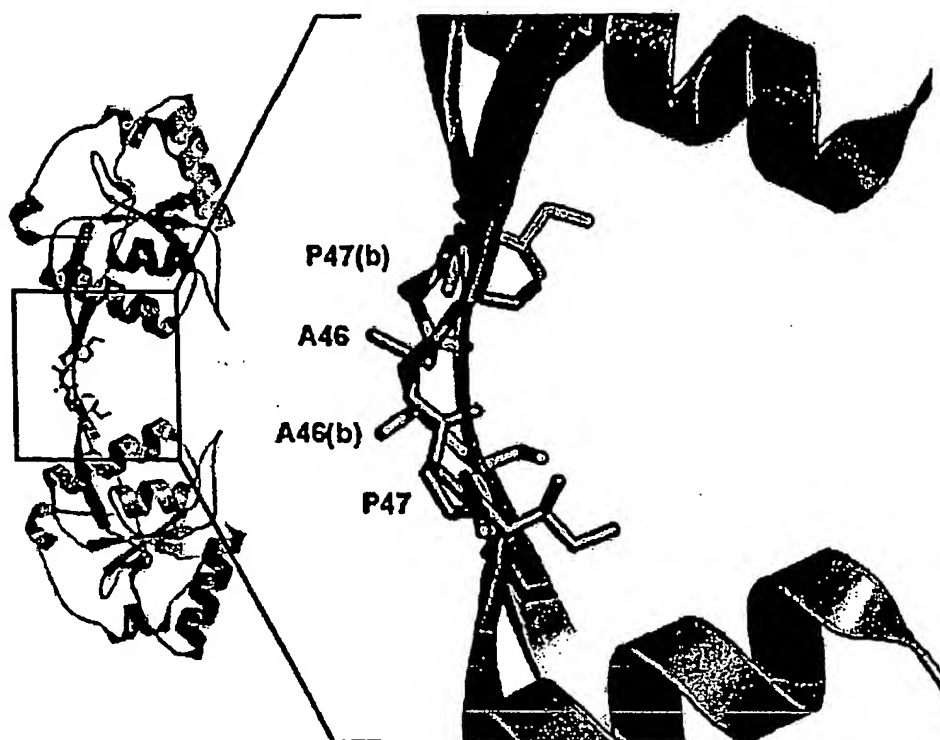


Figure 12

Figure 13

T7_endo1

>gi|431187:10257-10706 gene 3, endonuclease

ATGGCAGGTTACGGCGCTAAAGGAATCCGAAAGGTTGGAGCGTTTCGCTCTGGCC
TAGAGGACAAGGTTTCAAAGCAGTTGGAATCAAAAGGTATTAAATTCGAGTATGAA
GAGTGGAAAGTGCCTTATGTAATTCCGGCGAGCAATCACACTTACACTCCAGACTT
CTTACTTCCAAACGGTATATTCGTTGAGACAAAGGGTCTGTGGGAAAGCGATGATA
GAAAGAAGCACTTATTAATTAGGGAGCAGCACCCCGAGCTAGACATCCGTATTGTC
TTCTCAAGCTCACGTACTAAGTTATACAAAGGTTCTCCAACGTCTTATGGAGAGTTC
TGCGAAAAGCATGGTATTAAGTTCGCTGATAAACTGATACCTGCTGAGTGGATAAA
GGAACCCAAGAAGGAGGTCCCCTTTGATAGATTAAAAAGGAAAGGAGGAAAGAAA
TAA (SEQ ID NO:1)

>gi|15581|emb|CAA24402.1| unnamed protein product [Enterobacteria
phage T7]

MAGYGAKGIRKVGAFRSGLEDKVSKQLESKGIKFEYEEWKVPYVIPASNHTYTPDFL
LPNGIFVETKGLWESDDRKKHLLIREQHPELDIRIVFSSRTKLYKGSPTSYPGEFCEK
HGIKFADKLIPAEWIKPEPKKEVPFDRDLKRKGGKK (SEQ ID NO:13)

Figure 14-1

>gi|37956656|gb|AAP33926.1| gene 3 [Enterobacteria phage T7]

MAGYGAKGIRKVGAFRSGLEDKVSKQLESKGIFEYEEWKVPYVIPASNHTYT
PDFLLPNGIFVETKGLWESDDRKKHLLIREQHPELDIRIVFSSSRTKLYKGSPTS
YGEFCEKHGIFADKLIPAEWIKEPKKEVPFDRLKRKGGKK (SEQ ID NO:12)

>gi|9627444|ref|NP_041972.1| endonuclease [Enterobacteria phage T7]

MAGYGAKGIRKVGAFRSGLEDKVSKQLESKGIFEYEEWKVPYVIPASNHTYT
PDFLLPNGIFVETKGLWESDDRKKHLLIREQHPELDIRIVFSSSRTKLYKGSPTS
YGEFCEKHGIFADKLIPAEWIKEPKKEVPFDRLKRKGGKK (SEQ ID NO:12)

>gi|119370|sp|P00641|ENRN_BPT7 Endodeoxyribonuclease I
(Endonuclease)

MAGYGAKGIRKVGAFRSGLEDKVSKQLESKGIFEYEEWKVPYVIPASNHTYT
PDFLLPNGIFVETKGLWESDDRKKHLLIREQHPELDIRIVFSSSRTKLYKGSPTS
YGEFCEKHGIFADKLIPAEWIKEPKKEVPFDRLKRKGGKK (SEQ ID NO:12)

>gi|67296|pir||NEBP37 endodeoxyribonuclease I (EC 3.1.21.-) -
phage T7

MAGYGAKGIRKVGAFRSGLEDKVSKQLESKGIFEYEEWKVPYVIPASNHTYT
PDFLLPNGIFVETKGLWESDDRKKHLLIREQHPELDIRIVFSSSRTKLYKGSPTS
YGEFCEKHGIFADKLIPAEWIKEPKKEVPFDRLKRKGGKK (SEQ ID NO:12)

Figure 14-2

>gi|15517|emb|CAA24345.1| unnamed protein product

[Enterobacteria phage T7]

MAGYGAKGIRKVGAFRSGLEDKVSKQLESKGIKFEYEEWKVPYVIPASNHTYT
PDFLLPNGIFVETKGLWESDDRKKHLLIREQHPELDIRIVFSSSRTKLYKGSPTS
YGEFCEKHGIKFADKLIPAEWIKEPKKEVPFDRLKRKGGKK (SEQ ID NO:12)

=====

>gi|37956869|gb|AAP34135.1| gene 3 [Enterobacteria phage T7]

MAGYSAKGIRKVGAFRSGLEDKVSKQLESKGIKFEYEEWKVPYVIPASNHTYT
PDFLLPNGIFVETKGLWESDDRKKHLLIRKQHPQLDIRIVFSSSRTKLYKGSPTS
YGEFCEKHGIKFADKLIPAEWIKEPKKEVPFDRLKRKGGKK (SEQ ID NO:24)

>gi|37956815|gb|AAP34082.1| gene 3 [Enterobacteria phage T7]

MAGYSAKGIRKVGAFRSGLEDKVSKQLESKGIKFEYEEWKVPYVIPASNHTYT
PDFLLPNGIFVETKGLWESDDRKKHLLIRKQHPQLDIRIVFSSSRTKLYKGSPTS
YGEFCEKHGIKFADKLIPAEWIKEPKKEVPFDRLKRKGGKK (SEQ ID NO:24)

=====

>gi|37956764|gb|AAP34032.1| gene 3 [Enterobacteria phage T7]

MVGYGKVGIRKVGAFRSGLEDKVSKQLESKGIKFEYEEWKVPYVIPASNHTYT
PDFLLPNGIFVETKGLWESDDRKKHLLIREQHPELDIRIVFSSSRTKLYKGSPTS
YGEFCEKHGIKFADKLIPAEWIKEPKKEVSFDRLKRKGGKK (SEQ ID NO:25)

Figure 14-3

>gi|37956712|gb|AAP33981.1| gene 3 [Enterobacteria phage T7]
MVGYGKVGIRKVGAFRSGLEDKVSKQLESKGIFKFEYEEWKVPYVIPASNHTYT
PDFLLPNGIFVETKGLWESDDRKKHLLIREQHPELDIRIVFSSSRTKLYKGSPTS
YGEFCEKHGKIFADKLIPAEWIKEPKKEVSFDRLKRKGGKK (SEQ ID NO:25)

=====

>gi|30387466|ref|NP_848275.1| endonuclease [Yersinia pestis phage
phiA1122]
MAGTYAARGIRKVGTFRSGLEDKVSKQLEGKGIKFDYELWKIPYVVPASNHVY
TPDFLLPNGIFIETKGLWESDDRKKHLLIREQFPELDRLVFSSSRTKLYKGSPT
SYGEWCEKHGILFADKLIPVEWLKEPKKEVPFDRLKQAKGGKK
(SEQ ID NO:13)

>gi|30314103|gb|AAP20511.1| endonuclease [Yersinia pestis phage
phiA1122]
MAGTYAARGIRKVGTFRSGLEDKVSKQLEGKGIKFDYELWKIPYVVPASNHVY
TPDFLLPNGIFIETKGLWESDDRKKHLLIREQFPELDRLVFSSSRTKLYKGSPT
SYGEWCEKHGILFADKLIPVEWLKEPKKEVPFDRLKQAKGGKK
(SEQ ID NO:13)

=====

Figure 14-4

>gi|9634009|ref|NP_052083.1| endonuclease [Bacteriophage
phiYeO3-12]

MAGAYAARGVRKVGAFRSGLEDKVSQLESKGIFDYELWRIPYVIPASDHLY
TPDFLLPNGIFIETKGLWDSDDRKKHLLIREQHPELDIRLVFSSSRSKLYKGSPT
SYAEWCEKHGILFADKLIPVEWLKEPKKEVPFDKFKTKKGVKKNG
(SEQ ID NO:14)

>gi|6599000|emb|CAB63604.1| endonuclease [Bacteriophage
phiYeO3-12]

MAGAYAARGVRKVGAFRSGLEDKVSQLESKGIFDYELWRIPYVIPASDHLY
TPDFLLPNGIFIETKGLWDSDDRKKHLLIREQHPELDIRLVFSSSRSKLYKGSPT
SYAEWCEKHGILFADKLIPVEWLKEPKKEVPFDKFKTKKGVKKNG
(SEQ ID NO:14)

=====

>gi|17570803|ref|NP_523312.1| endonuclease [Bacteriophage T3]

MAGAYAARCTQGRAFRSGLEDKVSQLESKGIFDYELWRIPYVIPESDHLYT
PDFLLPNGIFIETKGLWDSDDRKKHLLIREQHPELDIRLVFSSSRSKLYKGSPTS
YGEWCEKHGILFADKLIPVAGVKEPKKEVPFDKFKTKKGVKKNG
(SEQ ID NO:15)

>gi|17384287|emb|CAC86275.1| endonuclease [Bacteriophage T3]

MAGAYAARCTQGRAFRSGLEDKVSQLESKGIFDYELWRIPYVIPESDHLYT
PDFLLPNGIFIETKGLWDSDDRKKHLLIREQHPELDIRLVFSSSRSKLYKGSPTS
YGEWCEKHGILFADKLIPVAGVKEPKKEVPFDKFKTKKGVKKNG
(SEQ ID NO:15)

Figure 14-5

>gi|119369|sp|P203|ENRN_BPT3 ENDODEOXYRIBONUCLEASE I
(ENDONUCLEASE)
MAGAYAARCTQGRAFRSGLEDKVSKQLESKGIKFDYELWRIPYVIPESDHLYT
PDFLLPNGIFIETKGLWDSDDRKKHLLIREQHPELDIRLVFSSSRSKLYKGSPTS
YGEWCEKHGILFADKLIPVAGVKEPKKEVPFDKFKTKKGVKKNG
(SEQ ID NO:15)

>gi|76916|pir||S07505 endodeoxyribonuclease I (EC 3.1.21.-) -
phage T3
MAGAYAARCTQGRAFRSGLEDKVSKQLESKGIKFDYELWRIPYVIPESDHLYT
PDFLLPNGIFIETKGLWDSDDRKKHLLIREQHPELDIRLVFSSSRSKLYKGSPTS
YGEWCEKHGILFADKLIPVAGVKEPKKEVPFDKFKTKKGVKKNG
(SEQ ID NO:15)

>gi|15694|emb|CAA35132.1| 3 [Bacteriophage T3]
MAGAYAARCTQGRAFRSGLEDKVSKQLESKGIKFDYELWRIPYVIPESDHLYT
PDFLLPNGIFIETKGLWDSDDRKKHLLIREQHPELDIRLVFSSSRSKLYKGSPTS
YGEWCEKHGILFADKLIPVAGVKEPKKEVPFDKFKTKKGVKKNG
(SEQ ID NO:15)

=====

Figure 14-6

>gi|29366712|ref|NP_813757.1| putative endonuclease

[Pseudomonas phage gh-1]

MAYAGPKGARTGAFRSGLEDNRNAKHMDKLGVKYDFERFHINYVVPARDAKYT
PDFVLANGIIIETKGIWEVDDRKKHLLIREQYPDLDIRLVFSNSNSKIYKGSPTS
YADFCTKHGIQFADKLVPRDWLKEARKEIPQGVLPKKGG (SEQ ID NO:16)

>gi|29243571|gb|AAO73150.1|AF493143_11 putative endonuclease

[Pseudomonas phage gh-1]

MAYAGPKGARTGAFRSGLEDNRNAKHMDKLGVKYDFERFHINYVVPARDAKYT
PDFVLANGIIIETKGIWEVDDRKKHLLIREQYPDLDIRLVFSNSNSKIYKGSPTS
YADFCTKHGIQFADKLVPRDWLKEARKEIPQGVLPKKGG (SEQ ID NO:16)

=====

>gi|26988992|ref|NP_744417.1| phage endodeoxyribonuclease I

[Pseudomonas putida KT2440]

MGLKYGFRSGLEERAADQLTAVGMGFTFESLVVPYTRPAKVH KYTPDFALANG
IIVETKGRFLTEDRQKQLLVKAQHPELDVRFVFSNSKTKINKRSTTTYADWCSK
NGFQYADKLVPHAWLNEPVNEASLSIIKGLSKEK (SEQ ID NO:17)

>gi|24983812|gb|AAN67881.1|AE016420_3 phage

endodeoxyribonuclease I [Pseudomonas putida KT2440]

MGLKYGFRSGLEERAADQLTAVGMGFTFESLVVPYTRPAKVH KYTPDFALANG
IIVETKGRFLTEDRQKQLLVKAQHPELDVRFVFSNSKTKINKRSTTTYADWCSK
NGFQYADKLVPHAWLNEPVNEASLSIIKGLSKEK (SEQ ID NO:17)

=====

Figure 14-7

>gi|9964626|ref|NP_064756.1| RP Endonuclease I [Roseophage
SIO1]

MLNSKSSTRKRALKAGYRSGLEEQTAKDLKKRKVLFTYEETKIKWLDSKVRTY
TPDFVLPNGVIIETKGRFVAADRRKHLEIQKQFGTLYDIRFVFTNSKAKLYKGAK
SSYADWCNKHGFLYADKTIPEDWLNE (SEQ ID NO:18)

>gi|9944317|gb|AAG02601.1|AF189021_20 Roseophage SIO1
complete genome

MLNSKSSTRKRALKAGYRSGLEEQTAKDLKKRKVLFTYEETKIKWLDSKVRTY
TPDFVLPNGVIIETKGRFVAADRRKHLEIQKQFGTLYDIRFVFTNSKAKLYKGAK
SSYADWCNKHGFLYADKTIPEDWLNE (SEQ ID NO:18)

=====

Figure 15

